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-1015 ATCACTGGTA TTAAAAAAAA ACACCTATGG TTTCCAAAAG ATTAAAACAA ACCAGCAGTT

-955 TTATAGAAGC TAACACTAAA ATCTAAAGGA ACTACGTTCT ATGGAGCCAC TTAATATGGA

-895 TAAACACTTT GACAATATTC TTTCAACAAC TACAGTAACA AGTTTCTTAG AGTCCATTTC

-835 TTTTTACATC CATAATGAAT TGTAAATCTT TTCTACTTCT TAAGTAAAAC ATCACCACTT

-775 AATTCTGGTA ACTTTTCCAT ATTAACTTTT TAGAACAATT GCAAACGTAC CATAAATGAT

-715 TGTTGTCACA GTGGTAACTA TTTGACCCTG ACTGTTATTT TGTATATAGC AGCTTTTAAA

-655 ATAAAAAGGC AACAAGTTTC TAGGCGTAAT TTCCACAGAT CTTTTATGTA AAACAATGAC

-595 ATCCTTTGCA ACTTCTGCCA TTTAATCTAT CTCAAGCAAG CTCTCTGGAA ACAAATCTAT

-535 TTGAAAGATT CTATTGTAAT TAGAAATCAG GGTAACTGAA TGCACTAGAT GAAAACCTTC

-475 TGACTGGGGC CAATGAAGTC AATAAAGTCA AAACTGCTGT GAATGCTCAA CTGTCTGCAG

-415 ATCAGATGTC TTGGGATGGA ATCCGTTCTC GAGGCCACCA TCATTAATAT CAATTTGGCC

-355 ATGTAATACA AGCCTCACTT GTTCCACTGT TACAAATGTG CTTAAAACTG AGCTCATTTA

-295 CAATCCAAAT ACATATGTAG GATGGTAACC AAGGCATCAC ACTAATTTAG GTATTATGTT

----------->

FP1 FP2

-235 TTAGGGGGAA CAAAAGGTAT GTTAATATTT TATTCATCTC CAAATTAACT ATAAATTGTG

FP3

-175 CATTCTTGCA TAGATCCTCC TTGGGAATGA GAAATTAGGA AAATCCAGTT GTTAAAATGA

FP4

-115 ATGCCTAAAA TCAAAATAAA ATTTGTTTTT CTGGCACCTG CTTGATGACA CAGACTAATA

---------- +1

-55 ACCAATGACA AAATTCCCTT GAACCCAAGT TTTCATTTCC TCCTATTGTG TGGTCAGGTT

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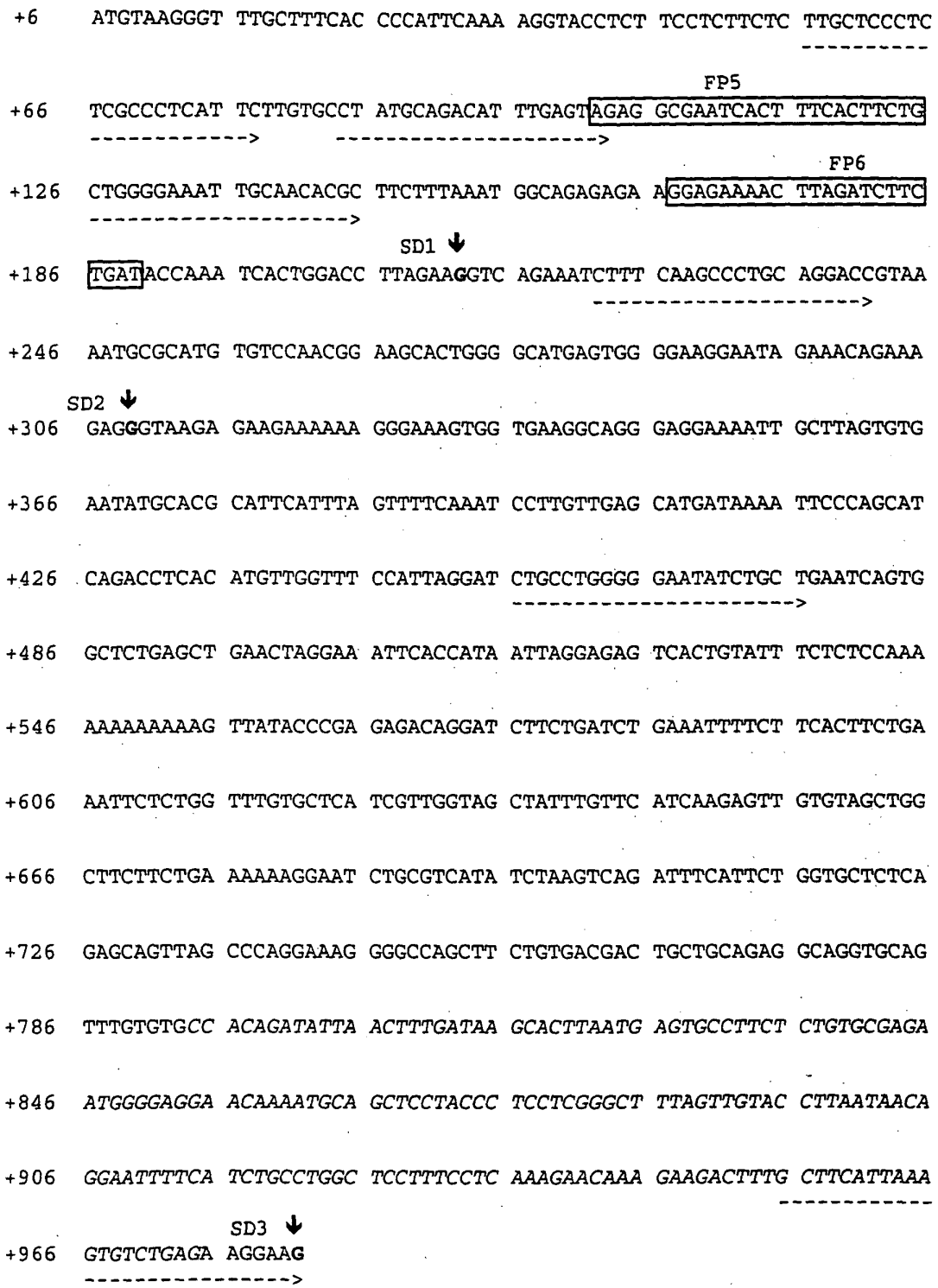
Fig. 1-1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FP5
+66 TCGCCCTCAT TCTTGTGCCT ATGCAGACAT TTGAGTAGAG GCGAATCACT TTCACTTCTG
FP6
+126 CTGGGGAAAT TGCAACACGC TTCTTTAAAT GGCAGAGAGA AGGAGAAAAC TTAGATCTTC
SD1
+186 TGATACCAAA TCACTGGACC TTAGAAGGTC AGAAATCTTT CAAGCCCTGC AGGACCGTAA
+246 AATGCGCATG TGTCCAACGG AAGCACTGGG GCATGAGTGG GGAAGGAATA GAAACAGAAA
SD2
+306 GAGGGTAAGA GAAGAAAAAA GGGAAAGTGG TGAAGGCAGG GAGGAAAATT GCTTAGTGTG
+366 AATATGCACG CATTCATTTA GTTTTCAAAT CCTTGTTGAG CATGATAAAA TTCCCAGCAT
+426 CAGACCTCAC ATGTTGGTTT CCATTAGGAT CTGCCTGGGG GAATATCTGC TGAATCAGTG
+486 GCTCTGAGCT GAACTAGGAA ATTCACCATA ATTAGGAGAG TCACTGTATT TCTCTCCAAA
+546 AAAAAAAAAG TTATACCCGA GAGACAGGAT CTTCTGATCT GAAATTTTCT TCACTTCTGA
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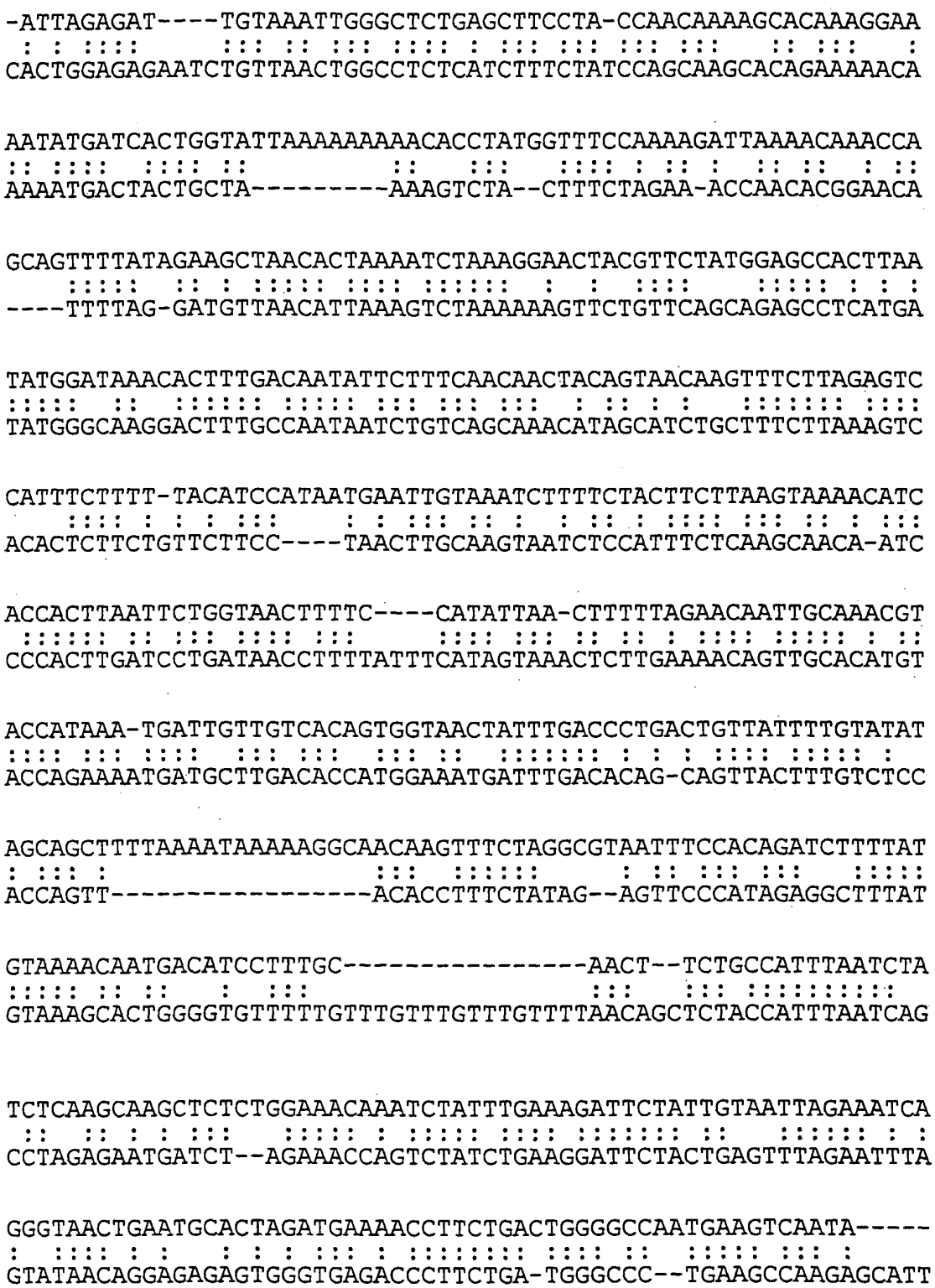
+666 CTTCTTCTGA AAAAAGGAAT CTGCGTCATA TCTAAGTCAG ATTTCATTCT GGTGCTCTCA
+726 GAGCAGTTAG CCCAGGAAAG GGGCCAGCTT CTGTGACGAC TGCTGCAGAG GCAGGTGCAG
+786 TTTGTGTGCC ACAGATATTA ACTTTGATAA GCACTTAATG AGTGCCTTCT CTGTGCGAGA
+846 ATGGGGAGGA ACAAAATGCA GCTCCTACCC TCCTCGGGCT TTAGTTGTAC CTTAATAACA
+906 GGAATTTTCA TCTGCCTGGC TCCTTTCCTC AAAGAACAAA GAAGACTTTG CTTCATTAAA
SD3
+966 GTGTCTGAGA AGGAAG

FIG. 1-2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AAAATGACTACTGCTA---------AAAGTCTA--CTTTCTAGAA-ACCAACACGGAACA
GCAGTTTTATAGAAGCTAACACTAAAATCTAAAGGAACTACGTTCTATGGAGCCACTTAA
----TTTTAG-GATGTTAACATTAAAGTCTAAAAAAGTTCTGTTCAGCAGAGCCTCATGA
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TATGGGCAAGGACTTTGCCAATAATCTGTCAGCAAACATAGCATCTGCTTTCTTAAAGTC
CATTTCTTTT-TACATCCATAATGAATTGTAAATCTTTTCTACTTCTTAAGTAAAACATC
ACACTCTTCTGTTCTTCC----TAACTTGCAAGTAATCTCCATTTCTCAAGCAACA-ATC
ACCACTTAATTCTGGTAACTTTTC----CATATTAA-CTTTTTAGAACAATTGCAAACGT
CCCACTTGATCCTGATAACCTTTTATTTCATAGTAAACTCTTGAAAACAGTTGCACATGT
ACCATAAA-TGATTGTTGTCACAGTGGTAACTATTTGACCCTGACTGTTATTTTGTATAT
ACCAGAAAATGATGCTTGACACCATGGAAATGATTTGACACAG-CAGTTACTTTGTCTCC
AGCAGCTTTTAAAATAAAAAGGCAACAAGTTTCTAGGCGTAATTTCCACAGATCTTTTAT
ACCAGTT-----------------ACACCTTTCTATAG--AGTTCCCATAGAGGCTTTAT
GTAAAACAATGACATCCTTTGC----------------AACT--TCTGCCATTTAATCTA
GTAAAGCACTGGGGTGTTTTTGTTTGTTTGTTTGTTTTAACAGCTCTACCATTTAATCAG
TCTCAAGCAAGCTCTCTGGAAACAAATCTATTTGAAAGATTCTATTGTAATTAGAAATCA
CCTAGAGAATGATCT--AGAAACCAGTCTATCTGAAGGATTCTACTGAGTTTAGAATTTA
GGGTAACTGAATGCACTAGATGAAAACCTTCTGACTGGGGCCAATGAAGTCAATA-----
GTATAACAGGAGAGAGTGGGTGAGACCCTTCTGA-TGGGCCC--TGAAGCCAAGAGCATT

Fig. 2-1

```
------------------AAGTCAAAA---------CTGCTGTGAATGCTCAACTGTCT
                  ::: ::: :         : ::: ::: ::: :::    :
GGCTCAGCTCTGAGTGCCCAAGCCAAGAGCATTGGCTCAGCTCTGAGTGCCCAAGCCATT

GCAGATCAGATGTCTTGGGATGGAATCCGTTCTCGAGGCCACCATCATTAATATCAATTT
::: : : : ::: :::: :::: :  :::: ::::::     : :  ::    :::
GCACA-CTGCTGTGTTGGCATGG---CGTTTCTGCAGGCCATTGGTACTCTTACTGTTTT

GGCCATGTAATACAAGCCTCACTTGTTCCACTGTTACAAATGTGCTTAAAACTGAGCTCA
:::::::::::: ::   :::::: ::: ::::: :::  :::::::::::: ::   ::
GGCCATGTAATTCATCGCTCACTA-TTCAACTGTGACAGGTGTGCTTAAAAC-GA---CA

TTTACAATCCAAATACATATGTAGGATGGTAACCAAGGCATCACACTAATTTAGGTATTA
:   :  : :: :  : :::     ::::: :::: : :     ::::: :: :   :::
TAC-CTGTTCACAGCC-TAT-----ATGGTGACCAGGACCCTGAACTAACTTGGACCTTA

TGTTTTAGGGGGAACAAAAGGTATGTTAATATTTTATTCATCTCCAAATT---AACTATA
:::   ::  : ::::::::  ::   :::::::: :: :: : ::::::   :: : ::
TGT--CAGAAGCAACAAAAGACATACCAATATTTTCTTGATTTTCAAATTGGTAAGT-TA

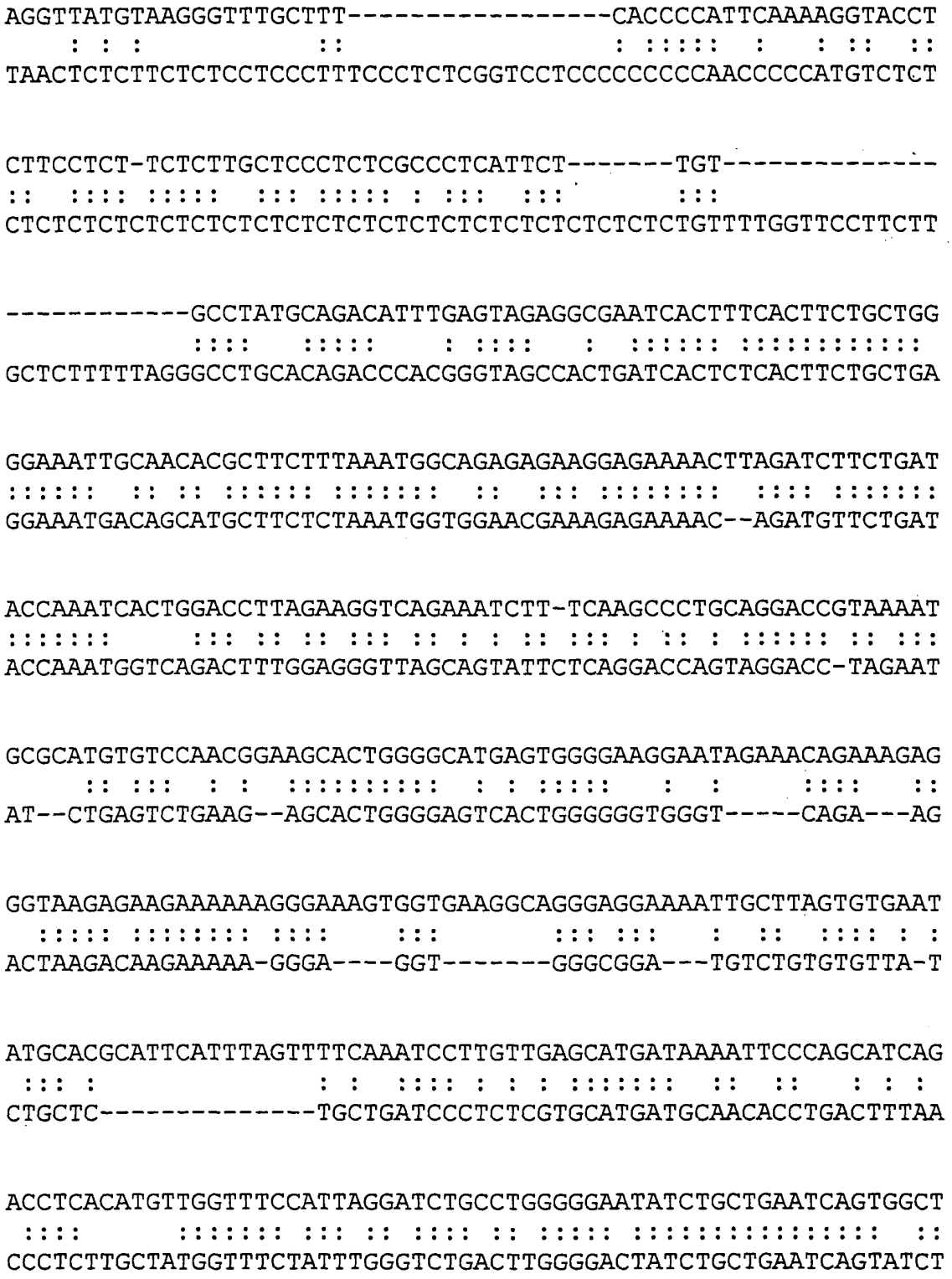
AATTGTGCATTCTTGCATAGATCCTCCTTGGGAATGAGAAATTAGGAAAATCCAGTTGTT
::::::  :  ::::: ::::: ::: :  ::       :::: :::::   :::::   :
AATTGTCTACCCTTGCGTAGATTCTCTTCAGGC-----AAATGAGGAAGTGCCAGT---T

AAAATGAATGCCTAAAATCAAAATAAAATTTGTTTTTCTGGCACCTGCTTGATGACACAG
:::   : ::  :::::::::::: :::: ::      :::::::::: ::::::   :
AAAGGTAGTGTGTAAAATCAAAACAAAAATTAAA---CTGGCACCTGCGTGATGAACAAA

ACTAATAACCAATGACAAAATTCCCTTGAACCCAAGTTTTCATTTCCTCCTAT-------
: : :::: ::::  : :: :  :: ::: ::  ::::::::::::: : ::
AATTATAATCAATGGTACAACTGTCT-GAAGTCA--TTTTCATTTCCTTCCATGAAGTGG

-------TGTGTGGTC
       :::: :: :
GCAGAGTTGTG-GGGC
```

Fig. 2-2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CTTCCTCT-TCTCTTGCTCCCTCTCGCCCTCATTCT-------TGT----------
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGTTTTGGTTCCTTCTT
----------GCCTATGCAGACATTTGAGTAGAGGCGAATCACTTTCACTTCTGCTGG
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GGAAATGACAGCATGCTTCTCTAAATGGTGGAACGAAAGAGAAAAC--AGATGTTCTGAT
ACCAAATCACTGGACCTTAGAAGGTCAGAAATCTT-TCAAGCCCTGCAGGACCGTAAAAT
ACCAAATGGTCAGACTTTGGAGGGTTAGCAGTATTCTCAGGACCAGTAGGACC-TAGAAT
GCGCATGTGTCCAACGGAAGCACTGGGGCATGAGTGGGGAAGGAATAGAAACAGAAAGAG
AT--CTGAGTCTGAAG--AGCACTGGGGAGTCACTGGGGGGTGGGT-----CAGA---AG
GGTAAGAGAAGAAAAAAGGGAAAGTGGTGAAGGCAGGGAGGAAAATTGCTTAGTGTGAAT
ACTAAGACAAGAAAAA-GGGA----GGT-------GGGCGGA---TGTCTGTGTGTTA-T
ATGCACGCATTCATTTAGTTTTCAAATCCTTGTTGAGCATGATAAAATTCCCAGCATCAG
CTGCTC--------------TGCTGATCCCTCTCGTGCATGATGCAACACCTGACTTTAA
ACCTCACATGTTGGTTTCCATTAGGATCTGCCTGGGGGAATATCTGCTGAATCAGTGGCT
CCCTCTTGCTATGGTTTCTATTTGGGTCTGACTTGGGGACTATCTGCTGAATCAGTATCT

Fig. 3-1

```
CTGAGCTGAACTAGGAAATTCACCATAATTAGGAGAGTCACTGTATT--------TCTCT
:::::: :::: : ::::::::::   :  ::  ::::::::::::        :::::
CTGAGCAGAACCAAGAAATTCACCCCCAA-AGAGGAGTCACTGTATTAGTCAGGGTCTCT

CCAAAAAAAAAAAAGTTATACCCGAGAGACAGGATCTTCTGATCTGAAATTTTCTTCACT
        :: ::::::: :::: ::: :::: ::: :::: ::::::::  ::: :
G-------AACAAAGTTAGACCCAAGAAACAGAATCCTCTGGTCTGAAATGGTCT-CTTG

TCTGAAATTCTCTGGTTTGTGCTCATCGTT----------GGTAGCTATTTGTTCATCA
: ::::::::::: :::::  : ::  :             :::::     :: :: :::
TGTGAAATTCTCTGCTTTGTACGCAAAGGAAAGAACATGCCGGTAGGAGCCTGCTCGTCA

A--GAGTTGTGTAGCTGGCTTCTTCTGAAAAAAGGAATCTGCGTCATATCTAAGTCAGAT
:  ::: :::: : :: :::::::::  :::::: :  :::::::: ::: ::: :::::
AACGAGGTGTGAATCTAGCTTCTTCTAGAAAAAGCAGCCTGCGTCACATCGAAGCCAGAT

TTCATTCTGGTGCTCTCAGAGCAGTTAGCCCAGGAAAGGGGCCAGCTTCTGTGACGACTG
::  ::::  :::::: ::::: ::::: : ::   :::: :  ::::: ::::: ::::
TTGGTTCTT-TGCTCTGAGAGCGGTTAGGCTAGTGGAGGG-CAGGCTTCCGTGACAACTG

CTGCAGAGGCAGGTGCAGTTTGTGTGCCACAGATATTAACTTTGATAAGCACTTAATGAG
 : ::: : :::::::::: :: :: :::::::::: :::: ::::::    :  :::::
GTACAGGGACAGGTGCAGTGTGGGTCCCACAGATATGAACTCTGATAAATCGTGCATGAG

TGCCTTCTCTGTGCGAGAATGGGGAGGAACAAAATGCAGCTCCTACCCTCCTCGGGCTTT
   :: ::::: :  ::::::: :: ::    :   ::::::: :::::::: ::: :
---CTACTCTGCGTAAGAATGGAGAAGAGAGCAGCCCAGCTCCCACCCTCCTGGGGTTCC

AGTTGTACCTTAATAACAGGAATTTTCATCTGCCTGGCTCCTTTCCTCAAAGAACAAAGA
  : : : : : ::            :::::::  : :: :  ::  : : ::: :
CATCGCAGCCTGAT-----------CATCTGCA-GCCTTC--TCAGCCAGGAAGATGTT

--AGACTTTGCTTCATTAAAGTGTCTGAGAAGGAAG
  :::   :::::: ::: :::::::: : ::::::
TCAGATCCTGCTTCGTTAGAGTGTCTG-GGAGGAAG
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Fig. 3-2

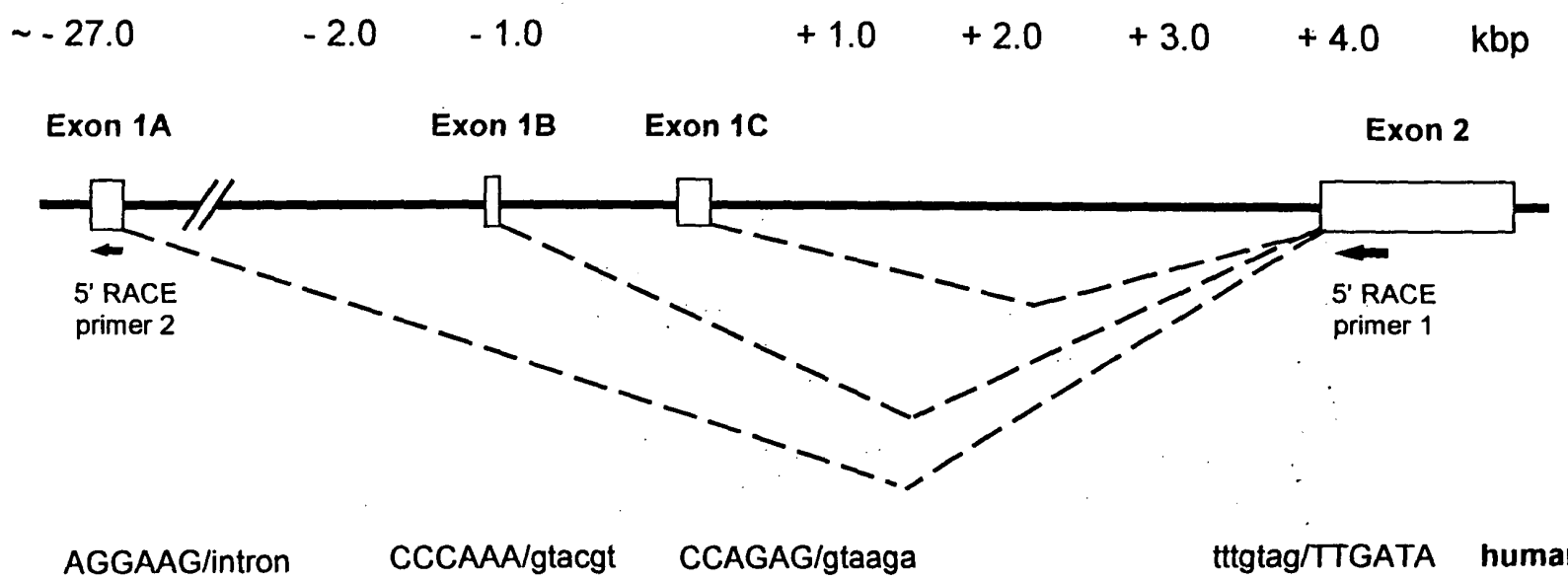

~ - 27.0
- 2.0
- 1.0
+ 1.0
+ 2.0
+ 3.0
+ 4.0
kbp
Exon 1A
Exon 1B
Exon 1C
Exon 2
5' RACE primer 2
5' RACE primer 1
AGGAAG/intron
CCCAAA/gtacgt
CCAGAG/gtaaga
tttgtag/TTGATA
human

Fig. 4

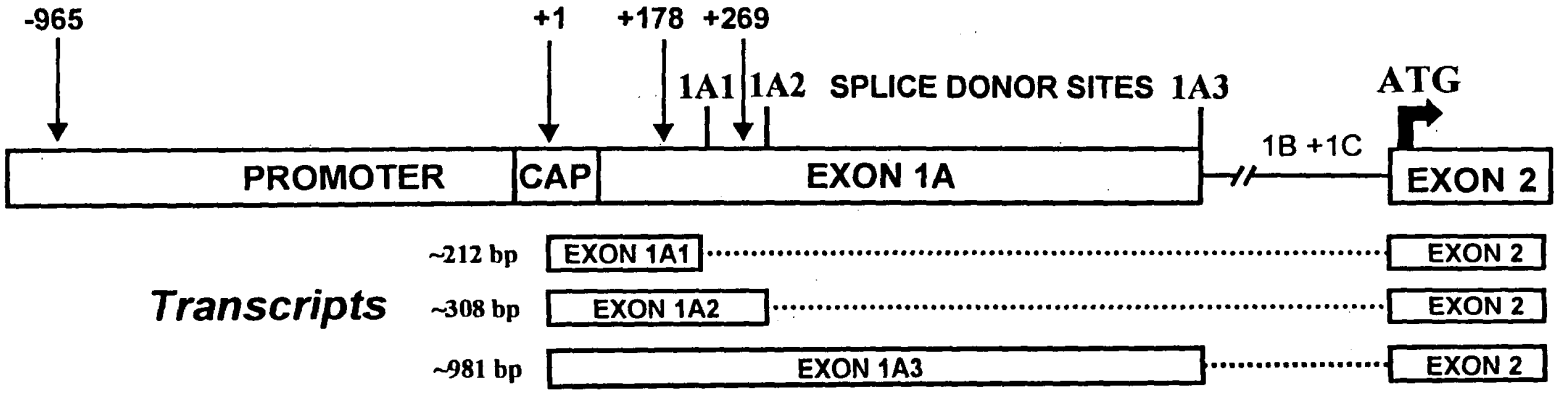

-965
+1
+178
+269
1A1
1A2
SPLICE DONOR SITES
1A3
ATG
1B +1C
PROMOTER
CAP
EXON 1A
EXON 2
Transcripts
~212 bp
EXON 1A1
EXON 2
~308 bp
EXON 1A2
EXON 2
~981 bp
EXON 1A3
EXON 2

Fig. 5

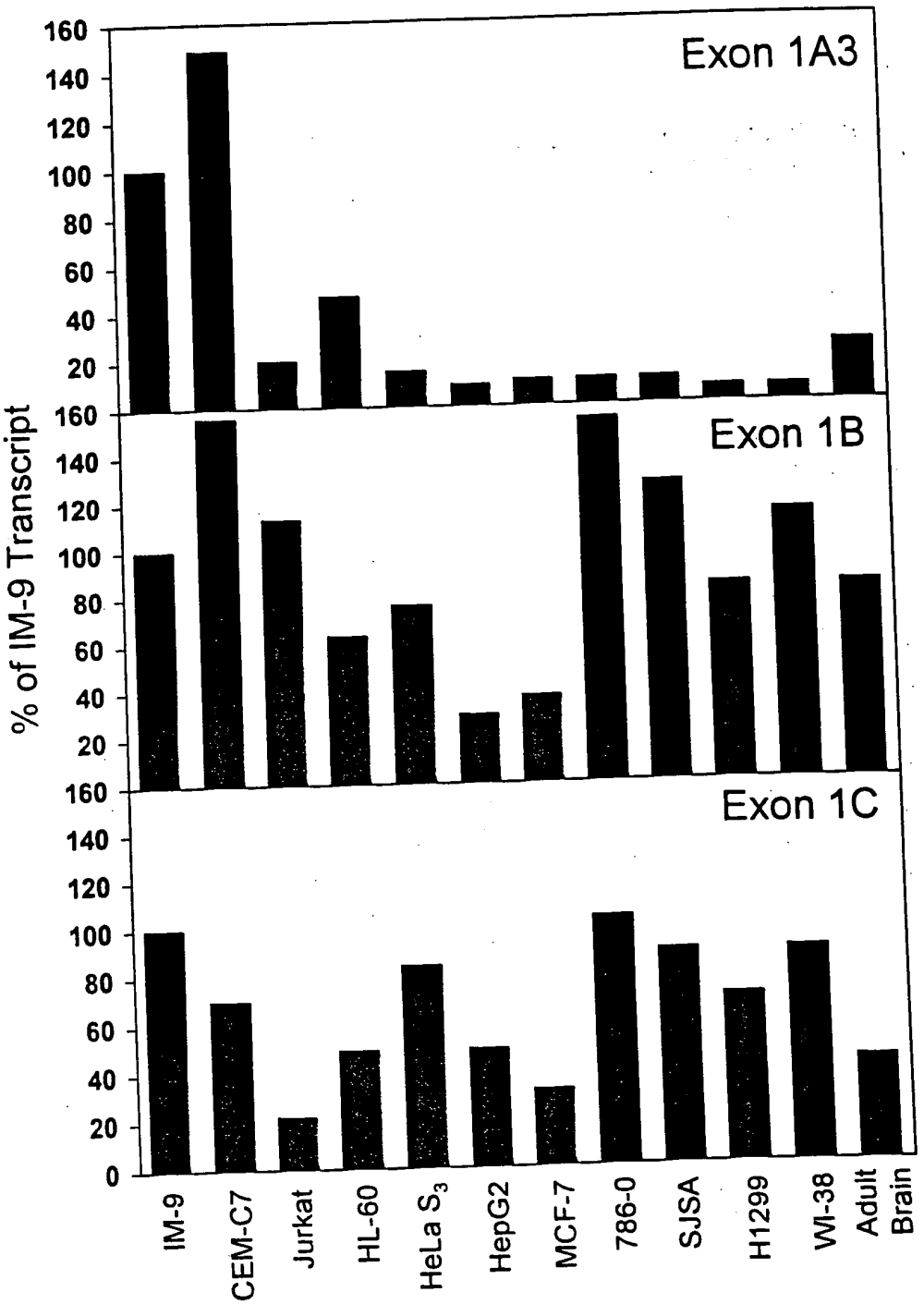

Exon 1A3
Exon 1B
Exon 1C
% of IM-9 Transcript
160
140
120
100
80
60
40
20
0
IM-9
CEM-C7
Jurkat
HL-60
HeLa S3
HepG2
MCF-7
786-0
SJSA
H1299
WI-38
Adult Brain

Fig. 6

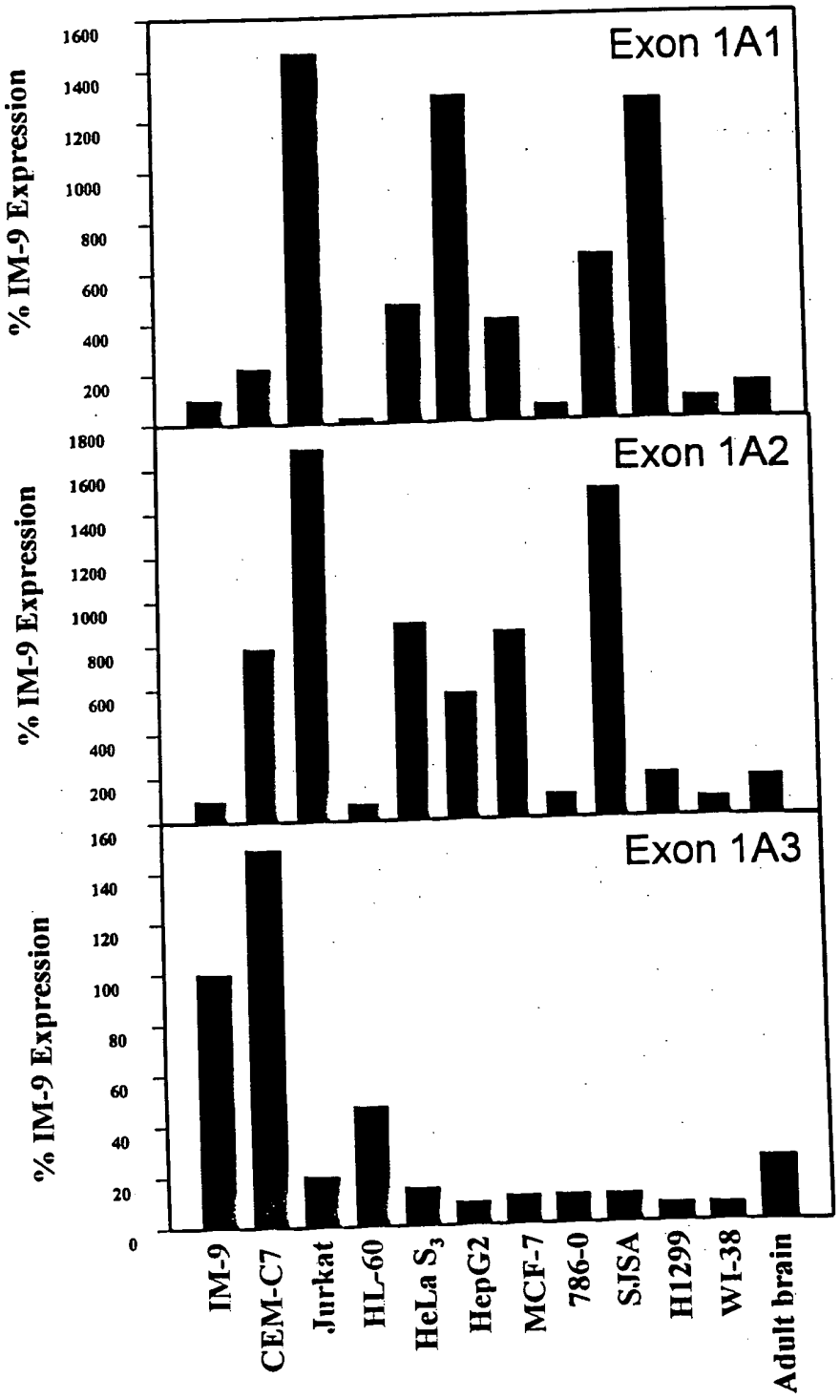

Exon 1A1
Exon 1A2
Exon 1A3
% IM-9 Expression
% IM-9 Expression
% IM-9 Expression
1600
1400
1200
1000
800
600
400
200
1800
1600
1400
1200
1000
800
600
400
200
160
140
120
100
80
60
40
20
0
IM-9
CEM-C7
Jurkat
HL-60
HeLa S3
HepG2
MCF-7
786-0
SJSA
H1299
WI-38
Adult brain

Fig. 7

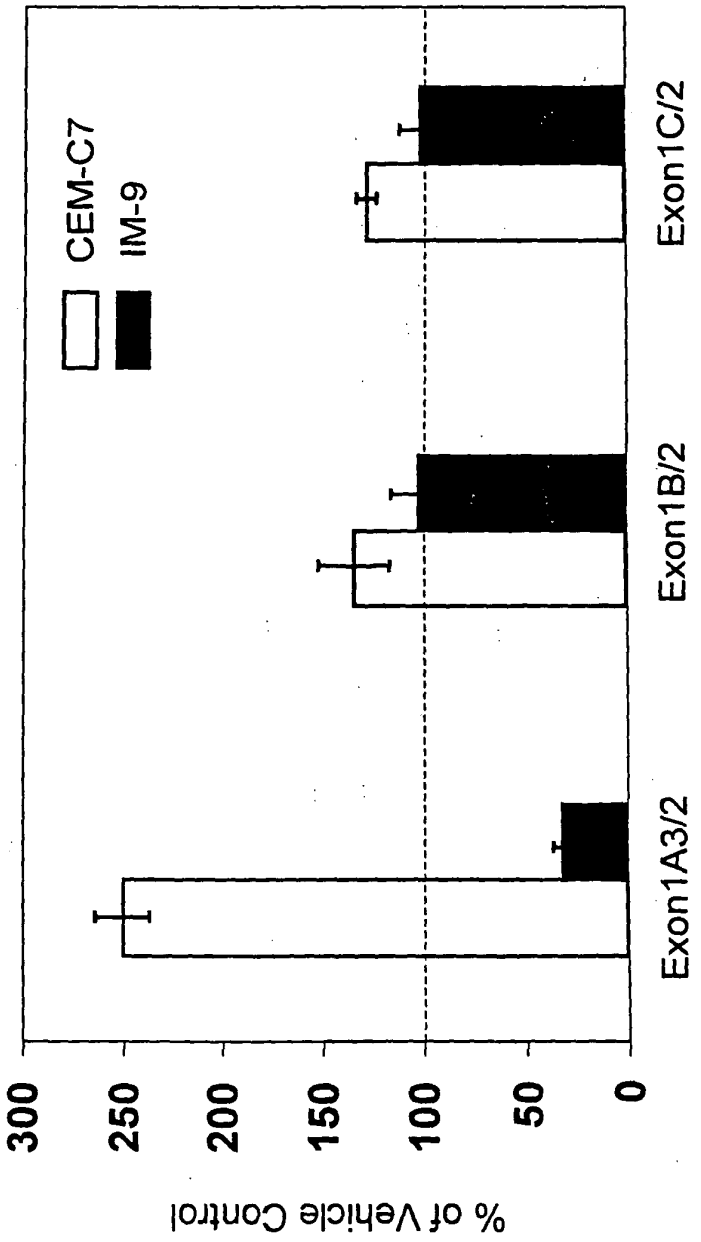

% of Vehicle Control
300
250
200
150
100
50
0
CEM-C7
IM-9
Exon1A3/2
Exon1B/2
Exon1C/2

Fig. 8

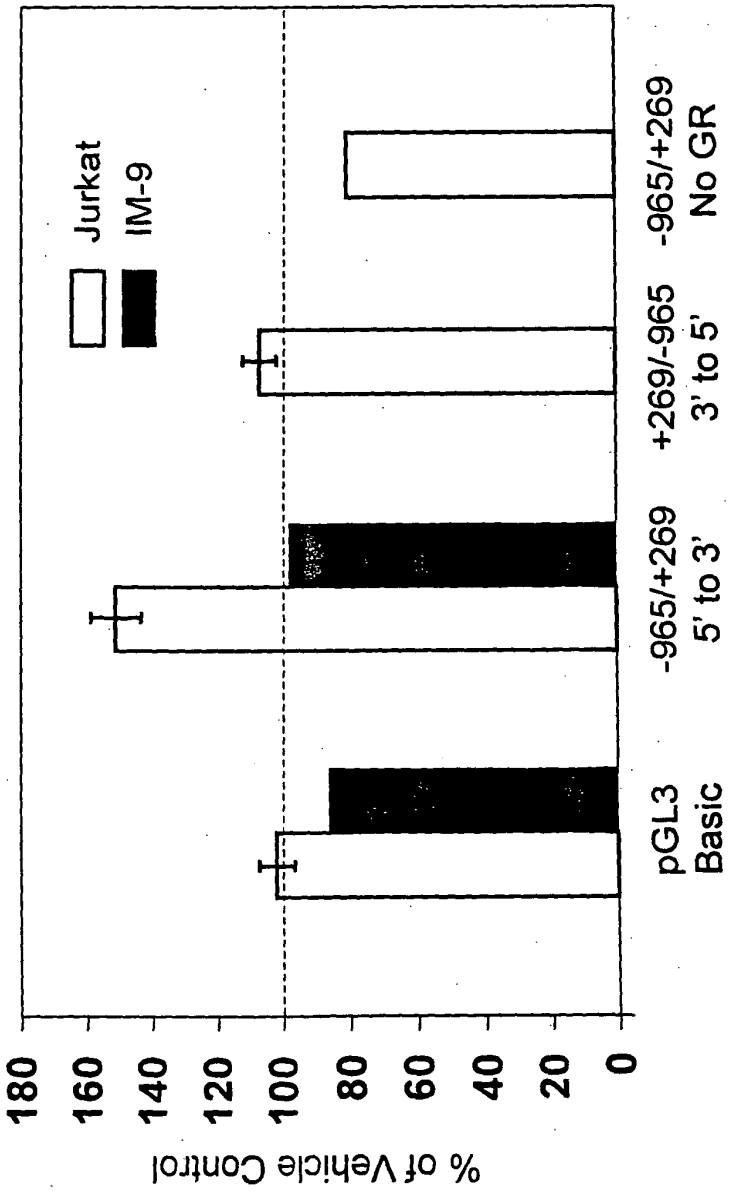
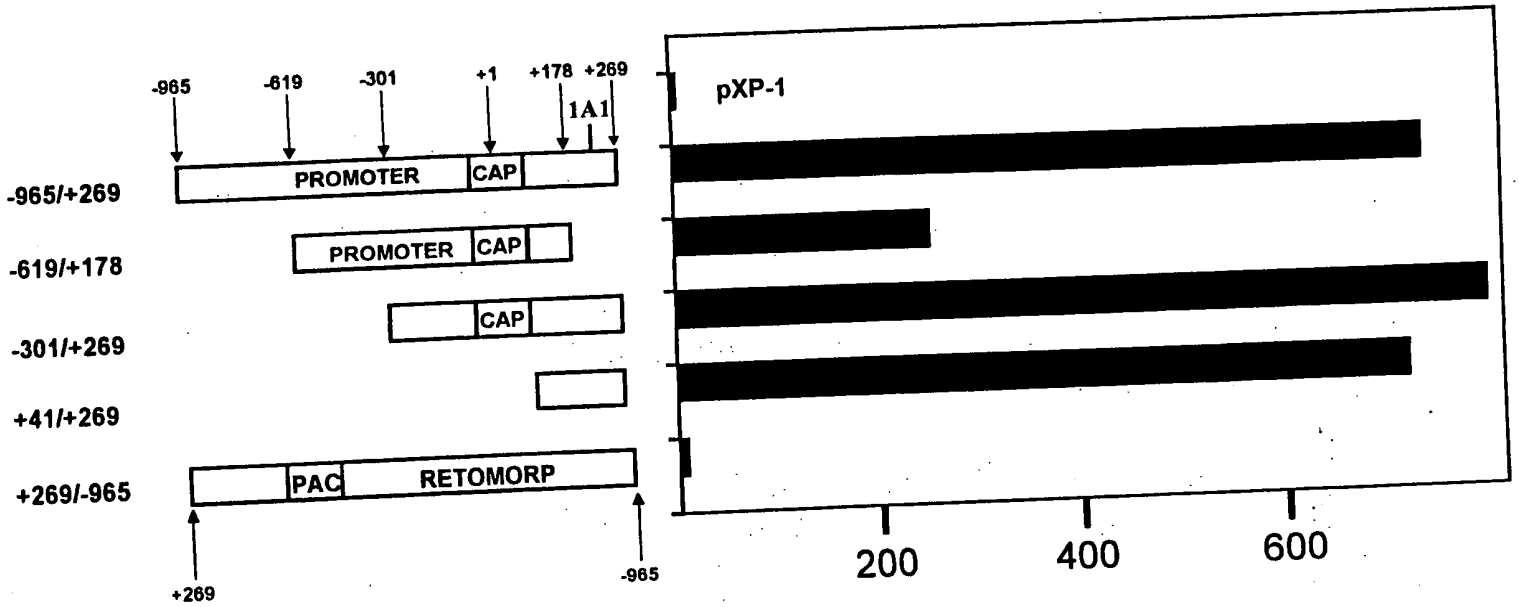

% of Vehicle Control
180
160
140
120
100
80
60
40
20
0
Jurkat
IM-9
pGL3 Basic
-965/+269 5' to 3'
+269/-965 3' to 5'
-965/+269 No GR

Fig. 9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-301
+1
+178
+269
1A1
PROMOTER
CAP
-965/+269
PROMOTER
CAP
-619/+178
CAP
-301/+269
+41/+269
PAC
RETOMORP
+269/-965
+269
-965
pXP-1
200
400
600
Relative Light Units (x 10^5)

Fig. 10

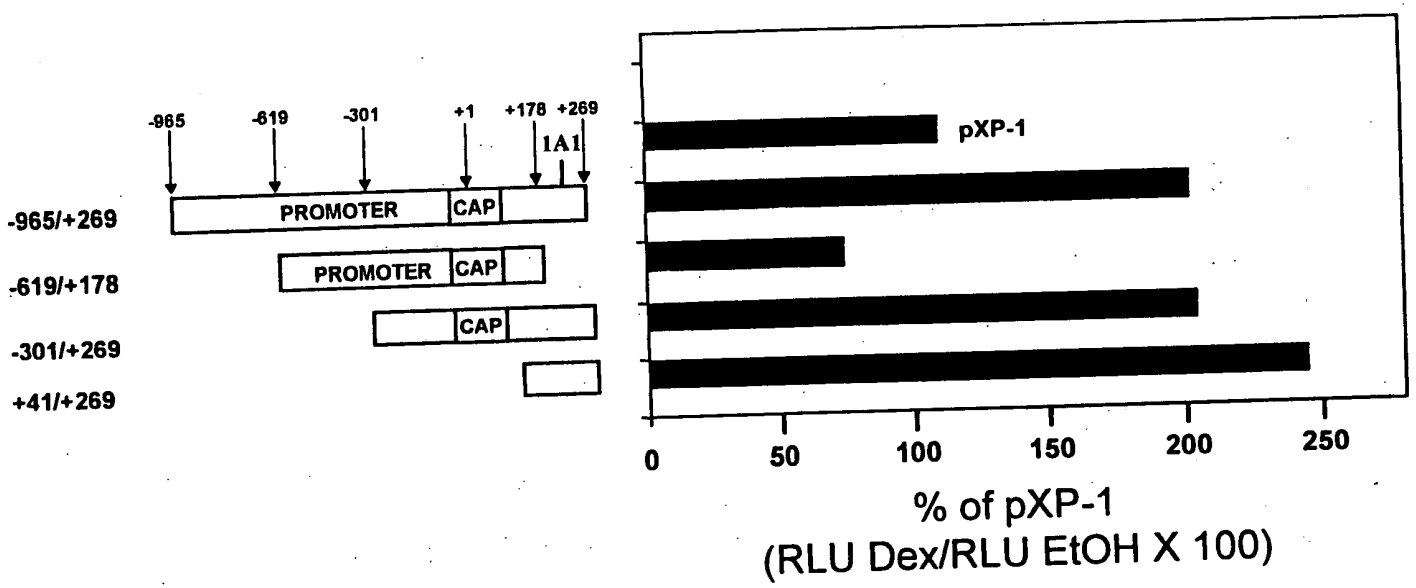
-965
-619
-301
+1
+178
+269
1A1
PROMOTER
CAP
-965/+269
-619/+178
-301/+269
+41/+269
pXP-1
0
50
100
150
200
250
% of pXP-1
(RLU Dex/RLU EtOH X 100)

Fig. 11

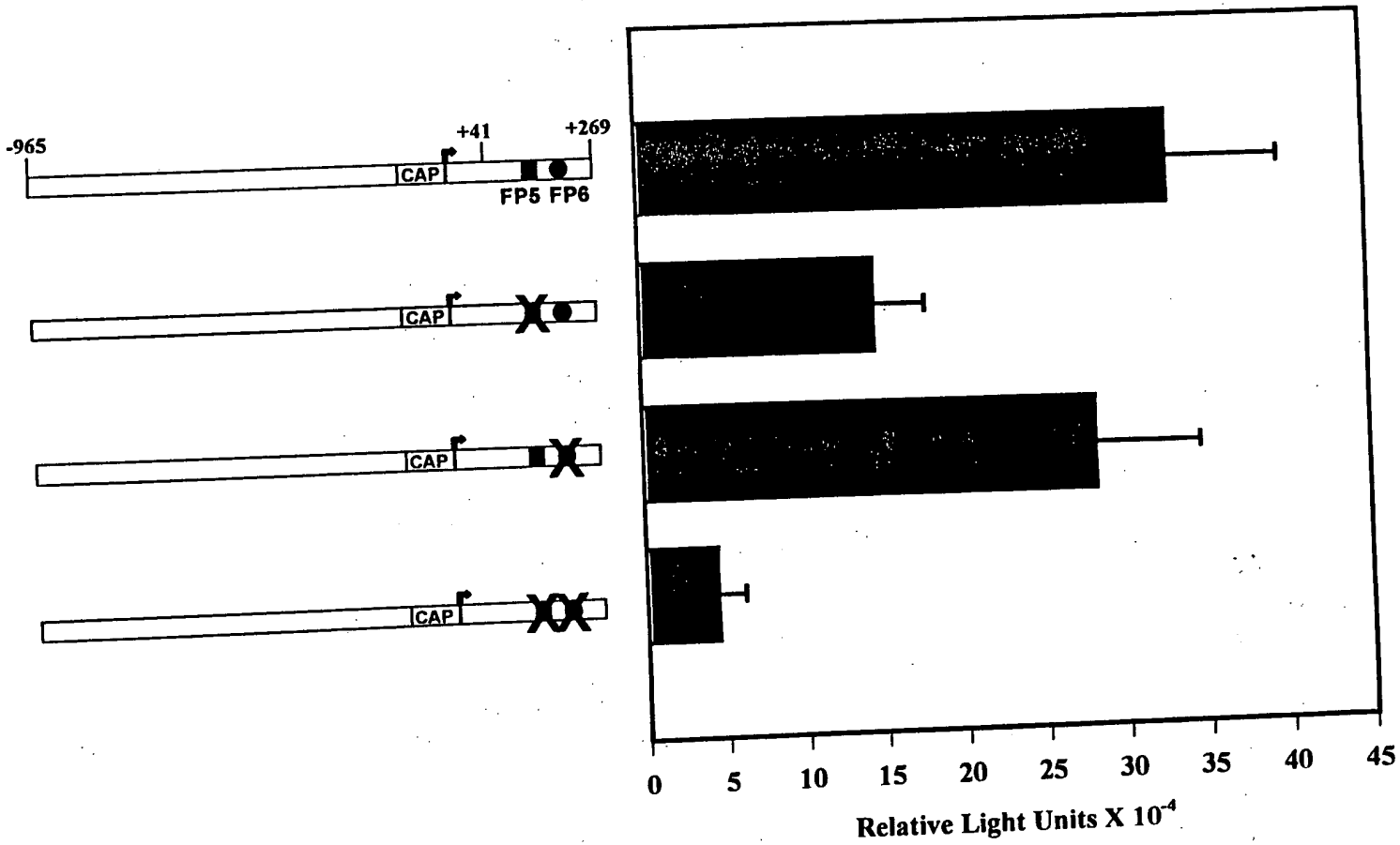
-965
+41
+269
CAP
FP5 FP6
CAP
CAP
CAP
0
5
10
15
20
25
30
35
40
45
Relative Light Units X 10-4

Fig. 12